

Title: US-10-787-267A-11

RESULT 11

AR204683

LOCUS AR204683 1503 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 6 from patent US 6368793.

ACCESSION AR204683

VERSION AR204683.1 GI:21502072

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1503)

AUTHORS Hoch, J. and Dartois, V.

TITLE Metabolic selection methods

JOURNAL Patent: US 6368793-A 6 09-APR-2002;

FEATURES Location/Qualifiers
source 1. 1503
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.3%; Score 34; DB 6; Length 1503;

Best Local Similarity 100.0%; Pred. No. 6e-06;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1467 ATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 1500

Db 1 ATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 34

Title: US-10-787-267A-11

RESULT 2

US-09-172-952-19

; Sequence 19, Application US/09172952

; Patent No. 6368793

; GENERAL INFORMATION:

; APPLICANT: Hoch, James

; APPLICANT: Dartois, Veronique

; TITLE OF INVENTION: METABOLIC SELECTION METHODS

; FILE REFERENCE: 234/191

; CURRENT APPLICATION NUMBER: US/09/172,952

; CURRENT FILING DATE: 1998-10-14

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 19

; LENGTH: 9334

; TYPE: DNA

; ORGANISM: yia

US-09-172-952-19

Query Match 100.0%; Score 1500; DB 3; Length 9334;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAAACAAGCACATAATAATAATCACCTTCATCACCAGAATATTTTAAATATTACGAG 60

Db 3750 CTAAAACAAGCACATAATAATAATCACCTTCATCACCAGAATATTTTAAATATTACGAG 3809

Qy 61 ACTATAAAGATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGG 120

Db 3810 ACTATAAAGATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGG 3869

Qy 121 TTAAGAATCATTCGCGCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAAT 180

Db 3870 TTAAGAATCATTCGCGCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAAT 3929

Qy	181	ATTGCCTTTGCGATGCCCCGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCG	240
Db	3930	ATTGCCTTTGCGATGCCCCGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCG	3989
Qy	241	GGGCTGGCGGGCGGTATTTTCTTTATCGGTTATCTATTTTACAGGTTCCCGCGCGGAAA	300
Db	3990	GGGCTGGCGGGCGGTATTTTCTTTATCGGTTATCTATTTTACAGGTTCCCGCGCGGAAA	4049
Qy	301	ATTGCCGTTTACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTC	360
Db	4050	ATTGCCGTTTACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTC	4109
Qy	361	ATCTCCGTGCTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTA	420
Db	4110	ATCTCCGTGCTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTA	4169
Qy	421	CTGGGCGTGGCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAAC TG GTTC	480
Db	4170	CTGGGCGTGGCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAAC TG GTTC	4229
Qy	481	CCCGACGCTGAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGG	540
Db	4230	CCCGACGCTGAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGG	4289
Qy	541	ATTATCACCGCCCCACTCTCAGGCTGGATTATCACGGTTC TCGACTGGCGCTGGCTGTTT	600
Db	4290	ATTATCACCGCCCCACTCTCAGGCTGGATTATCACGGTTC TCGACTGGCGCTGGCTGTTT	4349
Qy	601	ATTATCGAAGGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGAC	660
Db	4350	ATTATCGAAGGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGAC	4409
Qy	661	CGTCCGCAGGAAGCGCGCTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTG	720
Db	4410	CGTCCGCAGGAAGCGCGCTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTG	4469
Qy	721	GCCGCGGAGCAAAAAGCCATTGCCGGCACCAGGTGAAAAACGCCTCTCTGAGCGCCGTT	780
Db	4470	GCCGCGGAGCAAAAAGCCATTGCCGGCACCAGGTGAAAAACGCCTCTCTGAGCGCCGTT	4529
Qy	781	CTCTCCGACAAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATT	840
Db	4530	CTCTCCGACAAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATT	4589
Qy	841	TACGGCTACACCCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGG	900
Db	4590	TACGGCTACACCCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGG	4649
Qy	901	CAGGTCGGCATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCTGTTT	960
Db	4650	CAGGTCGGCATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCTGTTT	4709
Qy	961	TCCTCCCTTTTCAGACCGAACC GG TAAACGCAAGCTGTTCTGCTGCGCTGATTGGC	1020
Db	4710	TCCTCCCTTTTCAGACCGAACC GG TAAACGCAAGCTGTTCTGCTGCGCTGATTGGC	4769
Qy	1021	TTCGCTCTGTGCATGTTCTGTGCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCC	1080
Db	4770	TTCGCTCTGTGCATGTTCTGTGCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCC	4829
Qy	1081	GCGCTGGTCGGCTGCGGATTCTTCTTGCAATCGGCGGCTGGCGTGTCTGGACCATCCCG	1140
Db	4830	GCGCTGGTCGGCTGCGGATTCTTCTTGCAATCGGCGGCTGGCGTGTCTGGACCATCCCG	4889
Qy	1141	GCACGTCTGTTT CAGCGCGAAATGGCGGGCGGCGCGCGGGGTTATCAACGCGCTTGGC	1200

Db	4890	GCACGTCTGTTTCAGCGCGGAAATGGCGGGCGGCGCGCGGGGTTATCAACGCGCTTGGC	4949
Qy	1201	AACCTCGGCGGATTTTGTGGCCCTTATGCGGTGCGGGTGCTGATCACGTTGTACAGCAAA	1260
Db	4950	AACCTCGGCGGATTTTGTGGCCCTTATGCGGTGCGGGTGCTGATCACGTTGTACAGCAAA	5009
Qy	1261	GACGCTGGCGTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTG	1320
Db	5010	GACGCTGGCGTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTG	5069
Qy	1321	CTGCCGGCGGAAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAAATCCACATAAACGC	1380
Db	5070	CTGCCGGCGGAAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAAATCCACATAAACGC	5129
Qy	1381	ACTGCGTAAACTCGAGCCCGGCGGCGCTGCGCCTGCCGGGCGCTGCGAAATATGCCGGGTT	1440
Db	5130	ACTGCGTAAACTCGAGCCCGGCGGCGCTGCGCCTGCCGGGCGCTGCGAAATATGCCGGGTT	5189
Qy	1441	CACCCGGTAACAATGAGATGCGAAAGATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG	1500
Db	5190	CACCCGGTAACAATGAGATGCGAAAGATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG	5249

Title: US-10-787-267A-11

RESULT 3
US-09-172-952-5
; Sequence 5, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: yia x2
US-09-172-952-5

Query Match 87.8%; Score 1317; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	70	ATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGGTTAAGAATC	129
Db	1	ATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGGTTAAGAATC	60
Qy	130	ATTCCGCCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAATATTGCCTTT	189
Db	61	ATTCCGCCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAATATTGCCTTT	120
Qy	190	GCGATGCCCCGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCGGGGCTGGCG	249
Db	121	GCGATGCCCCGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCGGGGCTGGCG	180
Qy	250	GGCGGTATTTTCTTTATCGGTTATCTATTTTACAGGTTCCCGGCGGGAAAATTGCCGTT	309
Db	181	GGCGGTATTTTCTTTATCGGTTATCTATTTTACAGGTTCCCGGCGGGAAAATTGCCGTT	240
Qy	310	CACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTCATCTCCGTG	369
Db	241	CACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTCATCTCCGTG	300

Qy	370	CTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTACTGGGCGTG	429
Db	301	CTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTACTGGGCGTG	360
Qy	430	GCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAACTGGTTCCTCCGACGCT	489
Db	361	GCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAACTGGTTCCTCCGACGCT	420
Qy	490	GAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGGATTATCACC	549
Db	421	GAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGGATTATCACC	480
Qy	550	GCCCCACTCTCAGGCTGGATTATCACGGTTCTCGACTGGCGCTGGCTGTTTATTATCGAA	609
Db	481	GCCCCACTCTCAGGCTGGATTATCACGGTTCTCGACTGGCGCTGGCTGTTTATTATCGAA	540
Qy	610	GGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGACCGTCCGCAG	669
Db	541	GGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGACCGTCCGCAG	600
Qy	670	GAAGCGCGCTGGATTTCGGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTGGCCGCGGAG	729
Db	601	GAAGCGCGCTGGATTTCGGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTGGCCGCGGAG	660
Qy	730	CAAAAAGCCATTGCCGGCACCAGGTTGAAAAACGCCTCTCTGAGCGCCGTTCTCTCCGAC	789
Db	661	CAAAAAGCCATTGCCGGCACCAGGTTGAAAAACGCCTCTCTGAGCGCCGTTCTCTCCGAC	720
Qy	790	AAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATTTACGGCTAC	849
Db	721	AAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATTTACGGCTAC	780
Qy	850	ACCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGGCAGGTCGGC	909
Db	781	ACCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGGCAGGTCGGC	840
Qy	910	ATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCTGTTTCTCCCTT	969
Db	841	ATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCTGTTTCTCCCTT	900
Qy	970	TCAGACCGAACCGGTAAACGCAAGCTGTTTCGTCTGCCTGCCGCTGATTGGCTTCGCTCTG	1029
Db	901	TCAGACCGAACCGGTAAACGCAAGCTGTTTCGTCTGCCTGCCGCTGATTGGCTTCGCTCTG	960
Qy	1030	TGCATGTTCTGTTCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCCGCGCTGGTC	1089
Db	961	TGCATGTTCTGTTCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCCGCGCTGGTC	1020
Qy	1090	GGCTGCGGATTCTTCTGCAATCGGCGGCTGGCGTGTCTGGACCATCCCGGCACGTCTG	1149
Db	1021	GGCTGCGGATTCTTCTGCAATCGGCGGCTGGCGTGTCTGGACCATCCCGGCACGTCTG	1080
Qy	1150	TTCAGCGCGGAAATGGCGGGCGGCGCGCGGGGTTATCAACGCGCTTGGCAACCTCGGC	1209
Db	1081	TTCAGCGCGGAAATGGCGGGCGGCGCGCGGGGTTATCAACGCGCTTGGCAACCTCGGC	1140
Qy	1210	GGATTTTGTGGCCCTTATGCGGTCGGGGTGCTGATCACGTTGTACAGCAAAGACGCTGGC	1269
Db	1141	GGATTTTGTGGCCCTTATGCGGTCGGGGTGCTGATCACGTTGTACAGCAAAGACGCTGGC	1200
Qy	1270	GTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTGCTGCCGGCG	1329
Db	1201	GTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTGCTGCCGGCG	1260
Qy	1330	AAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAAATCCACATAAACGCACTGCG	1386

Title: US-10-787-267A-11

RESULT 10
 US-09-902-540-627
 ; Sequence 627, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 627
 ; LENGTH: 4835
 ; TYPE: DNA
 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-627

Query Match 1.4%; Score 21; DB 3; Length 4835;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 233 CCATGGCGGGGCTGGCGGGCG 253
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 Db 1546 CCATGGCGGGGCTGGCGGGCG 1566

Title: US-10-787-267A-11

RESULT 10
 AQ183262
 LOCUS AQ183262 402 bp DNA linear GSS 01-NOV-1998
 DEFINITION HS_3140_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3140 Col=24 Row=N, genomic survey sequence.
 ACCESSION AQ183262
 VERSION AQ183262.1 GI:3580629
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3140 row: N column: 24
 Class: BAC ends
 High quality sequence stop: 402.

FEATURES
 source
Location/Qualifiers
1. .402
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3140 Col=24 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match 1.4%; Score 21; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 ATATAACCTCTAACTCTACAA 94
 |||||
Db 104 ATATAACCTCTAACTCTACAA 124

US-10-787-267A-12

RESULT 1

US-09-172-952-14

; Sequence 14, Application US/09172952

~~; Patent No. 6368793~~

; GENERAL INFORMATION:

; APPLICANT: Hoch, James

; APPLICANT: Dartois, Veronique

; TITLE OF INVENTION: METABOLIC SELECTION METHODS

; FILE REFERENCE: 234/191

; CURRENT APPLICATION NUMBER: US/09/172,952

; CURRENT FILING DATE: 1998-10-14

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;  NUMBER OF SEQ ID NOS: 33
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; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 14

; LENGTH: 439

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; TYPE: PRT
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; ORGANISM: YiaX2
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US-09-172-952-14

Query Match 100.0%; Score 2254; DB 2; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNITSNSTTKDIPRQRLRIIPPILITCIISYMDRVNIAFAMPGGMDADLGISATMAGLA	60
Db	1	MNITSNSTTKDIPRQRLRIIPPILITCIISYMDRVNIAFAMPGGMDADLGISATMAGLA	60
Qy	61	GGIFFIGYLFQVPGGKIAVHSGGKFIGWSLVAWAVISVLTGLITNQYQLLALRFLLG	120
Db	61	GGIFFIGYLFQVPGGKIAVHSGGKFIGWSLVAWAVISVLTGLITNQYQLLALRFLLG	120
Qy	121	AEGGMLPVVLTMTISNWFPAERGRANAIVIMFVPIAGIITAPLSGWIITVLDWRWLFIE	180
Db	121	AEGGMLPVVLTMTISNWFPAERGRANAIVIMFVPIAGIITAPLSGWIITVLDWRWLFIE	180
Qy	181	GLLSLVVLVLWAYTIYDRPQEARWISEAEKRYLVETLAAEQKAIAGTEVKNASLSAVLSD	240
Db	181	GLLSLVVLVLWAYTIYDRPQEARWISEAEKRYLVETLAAEQKAIAGTEVKNASLSAVLSD	240
Qy	241	KTMWQLIALNFFYQTGIYGYTLWLPTILKELTHSSMGQVGMLAILPYVGAIAGMFLFSSL	300
Db	241	KTMWQLIALNFFYQTGIYGYTLWLPTILKELTHSSMGQVGMLAILPYVGAIAGMFLFSSL	300
Qy	301	SDRTGKRKLFVCLPLIGFALCMFLSVALKNQIWLSYAALVGCFFLQSAAGVFWTIPARL	360
Db	301	SDRTGKRKLFVCLPLIGFALCMFLSVALKNQIWLSYAALVGCFFLQSAAGVFWTIPARL	360
Qy	361	FSAEMAGGARGVINALGNLGGFCGPYAVGVLTITLYSKDAGVYCLAISLALAALMALLLPA	420
Db	361	FSAEMAGGARGVINALGNLGGFCGPYAVGVLTITLYSKDAGVYCLAISLALAALMALLLPA	420
Qy	421	KCDAGAAPVKTNPHKRTA	439
Db	421	KCDAGAAPVKTNPHKRTA	439